

O I P E

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/898,165

DATE: 07/24/2001  
TIME: 10:44:59

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\07242001\1898165.raw

ENTERED

4 <110> APPLICANT: Daniel H. Cohn  
5 Muhammad Faiyaz ul Haque  
6 Lily M. King  
7 Deborah Krakow  
9 <120> TITLE OF INVENTION: 3-PHOSPHOADENOSINE-5-PHOSPHOSULFATE  
10 (PAPS) SYNTHETASE PROTEINS AND METHODS FOR TREATING  
11 OSTEOARTHRITIC DISORDERS  
13 <130> FILE REFERENCE: 18810-81552  
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/898,165  
16 <141> CURRENT FILING DATE: 2001-07-02  
18 <150> PRIOR APPLICATION NUMBER: 09/399,212  
19 <151> PRIOR FILING DATE: 1999-09-17  
21 <160> NUMBER OF SEQ ID NOS: 28  
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 2014  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Homo sapiens  
30 <400> SEQUENCE: 1  
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32 ctccggcga gccagccagc atgtcgggga tcaagaagca aaagacggag aaccagcaga 120  
33 aatccaccaa tggatgttat caggcccacc atgtgagcag gaataagaga gggcaagtgg 180  
34 ttggacaacaag ggggtgggttc cgaggatgtc cctgtgtggct aacaggcttc tctgtgtctg 240  
35 gaaaaacaac gataagttt gcccctggagg agtaccttgc ctcccatgcc atcccttgtt 300  
36 actccctgga tggggacaat gtccgtcatg gccttaacag aaatctcgga ttctctcctg 360  
37 gggacagaga ggaaaatatac cgccggattt ctgaggtggc taagctgttt gctgtatgtg 420  
38 gtctggcttg cattaccagc ttatttttc cattcgcaaa ggatcgtgag aatgcccga 480  
39 aaatacatga atcagcaggg ctgccatttc ttgaaatatt tggatgtca cctctaaata 540  
40 tttgtgaaag cagagacgtt aaaggctct ataaaaggc cagagctggg gagattaaag 600  
41 gatttacagg tattgatttc gattatgaga aacctgaaac tcctgagcgt gtgtttaaaa 660  
42 ccaatttgc cacagtgtt gactgtgtcc accaggttgtt ggaacttctg caagagcaga 720  
43 acattgtacc ctataactata atcaaagata tccacgaact ctttgtccg gaaaacaaac 780  
44 ttgaccacgt ccgagcttag gctgaaaactc tcccttcatt atcaattact aagctggatc 840  
45 tccagttgggt ccaggtttt agcgaaggct gggccactcc cctcaaaagggt ttcatgcggg 900  
46 agaaggagta cttacaggtt atgcactttt acaccctgtt agatgtatggc gtgtatcaaca 960  
47 tgagcatccc cattgtactt cccgtctctg cagaggataa gacacggctg gaagggtgca 1020  
48 gcaagtttgtt cctggcacat ggtggacgga gggtagctat cttacagac gctgaattct 1080  
49 atgaacacag aaaagaggaa cgctgttccc gtgtttgggg gacaacatgt aaaaaacacc 1140  
50 cccatatacaa aatggtgatg gaaagtgggg actggcttgtt tggtggagac cttcagggtgc 1200  
51 tggagaaaat aagatggaaat gatgggctgg accaataccg tctgacaccc ctggagctca 1260  
52 aacagaaaatg taaagaaaatg aatgtgtatg cgggttttc attccagttt cgcacatcc 1320  
53 tccacaatgg ccatgccctg ttgtatgcagg acacctggc caggtccata gagaggggtc 1380  
54 acaagcaccc ggtcctccata ctacaccctc tggcggctg gaccaaggat gacgtatgtc 1440  
55 ctctagactg gcggtatggcag cagcacgcgg ctgtgtctca ggaagggttc ctggatccca 1500  
56 agtcaaccat tggatgtatc ttccgtctc ccatgttata tgctggcccc acagaggtcc 1560  
57 agtggcactg caggtcccgg atgattgcgg gtgccaattt ctacattgtg gggagggacc 1620  
58 ctgcaggaat qccccatctt qaaaccaaaq aqgatctqta tqaacccact catqqqqqca 1680

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59 aggtcttgag catggccctt ggcctcacct ctgtggaaat cattccattc cgagtggctg 1740  
 60 cctacaacaa agccaaaaaa gccatggact tctatgatcc agcaaggcac aatgagttt 1800  
 61 acttcatctc aggaactcga atgaggaagc tcgcccggga aggagagaat ccccccagatg 1860  
 62 gcttcatggc ccccaaaagca tgaagggtcc tgacagatta ttacaggtcc ctggagaaga 1920  
 63 actaaggcctt tgggtccaga gtttcttctt gaagtgcctt ttgattacct tttcttatttt 1980  
 64 tatgattaga tgctttgtat taaattgctt ctca 2014  
 66 <210> SEQ ID NO: 2  
 67 <211> LENGTH: 2000  
 68 <212> TYPE: DNA  
 69 <213> ORGANISM: Mus musculus  
 71 <400> SEQUENCE: 2  
 72 gtattctcaa catcagatat catgtcttgg aggaagttac ctaaactctg aagaattatc 60  
 73 atgtctgcaa atttcaaaat gaaccataaa agagaccagc aaaaatccac caatgtggtc 120  
 74 taccaggccc atcatgtgag caggaacaag agaggacaag tgggtggaaac caggggagga 180  
 75 ttccgaggat gtaccgtgtg gctaacaggc ctctctggc ctggggaaac aaccataagc 240  
 76 tttgctttgg aagagtacct tttatctcac gccatcccat gttactccct ggatggggac 300  
 77 aatgtccgtc atggccttaa taagaacctg ggattctctg ccggggaccc agaagagaat 360  
 78 atccggccgga tgcggaggt ggcacagtc tttgcgacg ccggcctggc ttgcacatcacc 420  
 79 agctttatct ctccctttgc aaaggatcgt gagaatgcac gaaaaatcca cgaatcagca 480  
 80 ggactccgt tctttgagat cttttagat ggcgccttaa atatctgtga aagccgagac 540  
 81 gtaaaaggac tctacaaacg agcccgagca ggagagatta aagggtttac aggcacatcgat 600  
 82 tctgactatg agaaacctga aactccagag tttgtgtctga agaccaactt gtcttcagta 660  
 83 agcactgtg tgcaacacagg tttgtggactt ttgcaggagc agaacattgt accccacacc 720  
 84 accatcaaag gcatccacga actctttgtg ccagaaaaca aagtgcacatca aatccgagct 780  
 85 gaggcagaga ctctcccatc actaccaatt accaagctgg atctgcagtg ggtgcagatt 840  
 86 ctgagtgaag gctggccac tcccctcaaa ggctttagtc gggagaagga atacttgcaa 900  
 87 actctacact tgcacactt actggacgat ggagtcatca acatgagttt tcccattgt 960  
 88 ttggccgttt ctgcggatga caaggcacgg ctcgaagggt gcagcaatt tgccttgatg 1020  
 89 tacgaaggcggc ggaggggtcgc tctattacag gaccctgaat tctatgagca taggaaagag 1080  
 90 gagcgttgtt ctgcgtgtg gggacacggc actgcacatc acccccatat caaaatggtg 1140  
 91 atgaaaatgt gggactggct tttttgtggc gacctacagg tgcttagagag aataagggtgg 1200  
 92 gacgatgggc tggaccaata ccgccttacg cctctggaaac tcaaacagaaa gtgtaaagac 1260  
 93 atgaatgtgtg atgcgtgtt tgcattccat ttgcgcataat ctgtccacaa tggtcatgcc 1320  
 94 ctctgtatgc aggacacccg ccgcaggctc ctggagaggg gttacaagca cccagtcctc 1380  
 95 ctgctccacc ctcttgggg ctggaccaag gacgatgacg tacctctggc atggaggatg 1440  
 96 aaacagcatg cagctgtact ggaggaaagg gtcctggatc ccaagtcaac tattttgccc 1500  
 97 atctttccat ctccatgtt atacgctggt cccacagagg tccagtggc ttgcagatgc 1560  
 98 cggatgattg caggagccaa ttctacattt gttggtaggg atcccgagg aatgccccat 1620  
 99 cctgagacaa agaaagaccc atatgaaccc acccacgggg gcaaggctt ggtatggcc 1680  
 100 cctggcccta cctctgtgg aataattccg ttccgagttt ctgcctacaa taaaattaaa 1740  
 101 aaggccatgg actttatgtt tccagcaagg cacgaggat ttgacttcat ctcaggaact 1800  
 102 cgcacatggc agctcgcccg ggaaggagaa gatccccat atggcttcat ggccccgaaa 1860  
 103 gctgtggaaag tttttttttt ttactacagg tctctggaga agaccaacta ggtgcctctg 1920  
 104 gctctggctt ctgcgtatgtt tgcgtatgtt cttttttttt tttttttttt tttttttttt 1980  
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 107 <210> SEQ ID NO: 3  
 108 <211> LENGTH: 20  
 109 <212> TYPE: DNA  
 110 <213> ORGANISM: Homo sapiens

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112 <400> SEQUENCE: 3  
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115 <210> SEQ ID NO: 4  
116 <211> LENGTH: 20  
117 <212> TYPE: DNA  
118 <213> ORGANISM: Homo sapiens  
120 <400> SEQUENCE: 4 20  
121 cgaaaaatgc gcaacaatgg  
123 <210> SEQ ID NO: 5  
124 <211> LENGTH: 20  
125 <212> TYPE: DNA  
126 <213> ORGANISM: Homo sapiens  
128 <400> SEQUENCE: 5 20  
129 ctggtgctgg aaaaacaacg  
131 <210> SEQ ID NO: 6  
132 <211> LENGTH: 22  
133 <212> TYPE: DNA  
134 <213> ORGANISM: Homo sapiens  
136 <400> SEQUENCE: 6 22  
137 tgcgaatgga gaaataaagc tg  
139 <210> SEQ ID NO: 7  
140 <211> LENGTH: 615  
141 <212> TYPE: PRT  
142 <213> ORGANISM: Homo sapiens  
144 <400> SEQUENCE: 7  
145 Met Ser Gly Ile Lys Lys Gln Lys Thr Glu Asn Gln Gln Lys Ser Thr  
146 1 5 10 15  
147 Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln  
148 20 25 30  
149 Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr  
150 35 40 45  
151 Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu Glu  
152 50 55 60  
153 Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn  
154 65 70 75 80  
155 Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg  
156 85 90 95  
157 Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala Asp  
158 100 105 110  
159 Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp  
160 115 120 125  
161 Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe  
162 130 135 140  
163 Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val  
164 145 150 155 160  
165 Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr  
166 165 170 175  
167 Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu  
168 180 185 190

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169 Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu  
 170 195 200 205  
 171 Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile  
 172 210 215 220  
 173 His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu  
 174 225 230 235 240  
 175 Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp  
 176 245 250 255  
 177 Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met  
 178 260 265 270  
 179 Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp  
 180 275 280 285  
 181 Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser Ala  
 182 290 295 300  
 183 Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His  
 184 305 310 315 320  
 185 Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His  
 186 325 330 335  
 187 Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys  
 188 340 345 350  
 189 His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly  
 190 355 360 365  
 191 Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp  
 192 370 375 380  
 193 Gln Tyr Arg Leu Thr Pro Leu Glu Leu Lys Gln Lys Cys Lys Glu Met  
 194 385 390 395 400  
 195 Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn  
 196 405 410 415  
 197 Gly His Ala Leu Leu Met Gln Asp Thr Cys Arg Arg Leu Leu Glu Arg  
 198 420 425 430  
 199 Gly Tyr Lys His Pro Val Leu Leu Leu His Pro Leu Gly Gly Trp Thr  
 200 435 440 445  
 201 Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala  
 202 450 455 460  
 203 Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile  
 204 465 470 475 480  
 205 Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His  
 206 485 490 495  
 207 Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg  
 208 500 505 510  
 209 Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu  
 210 515 520 525  
 211 Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser  
 212 530 535 540  
 213 Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys  
 214 545 550 555 560  
 215 Ala Met Asp Phe Tyr Asp Pro Ala Arg His Asn Glu Phe Asp Phe Ile  
 216 565 570 575  
 217 Ser Gly Thr Arg Met Arg Lys Leu Ala Arg Glu Gly Glu Asn Pro Pro

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218 580 585 590  
219 Asp Gly Phe Met Ala Pro Lys Ala Trp Lys Val Leu Thr Asp Tyr Tyr  
220 595 600 605  
221 Arg Ser Glu Met Asp Lys Asn  
222 610 615  
225 <210> SEQ ID NO: 8  
226 <211> LENGTH: 617  
227 <212> TYPE: PRT  
228 <213> ORGANISM: Mus musculus  
230 <400> SEQUENCE: 8  
231 Met Ser Ala Asn Phe Lys Met Asn His Lys Arg Asp Gln Gln Lys Ser  
232 1 5 10 15  
233 Thr Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly  
234 20 25 30  
235 Gln Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu  
236 35 40 45  
237 Thr Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu  
238 50 55 60  
239 Glu Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp  
240 65 70 75 80  
241 Asn Val Arg His Gly Leu Asn Lys Asn Leu Gly Phe Ser Ala Gly Asp  
242 85 90 95  
243 Arg Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala  
244 100 105 110  
245 Asp Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys  
246 115 120 125  
247 Asp Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe  
248 130 135 140  
249 Phe Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp  
250 145 150 155 160  
251 Val Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe  
252 165 170 175  
253 Thr Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Cys Val  
254 180 185 190  
255 Leu Lys Thr Asn Leu Ser Ser Val Ser Asp Cys Val Gln Gln Val Val  
256 195 200 205  
257 Glu Leu Leu Gln Glu Gln Asn Ile Val Pro His Thr Thr Ile Lys Gly  
258 210 215 220  
259 Ile His Glu Leu Phe Val Pro Glu Asn Lys Val Asp Gln Ile Arg Ala  
260 225 230 235 240  
261 Glu Ala Glu Thr Leu Pro Ser Leu Pro Ile Thr Lys Leu Asp Leu Gln  
262 245 250 255  
263 Trp Val Gln Ile Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe  
264 260 265 270  
265 Met Arg Glu Lys Glu Tyr Leu Gln Thr Leu His Phe Asp Thr Leu Leu  
266 275 280 285  
267 Asp Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser  
268 290 295 300  
269 Ala Asp Asp Lys Ala Arg Leu Glu Gly Cys Ser Lys Phe Ala Leu Met

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/898,165

DATE: 07/24/2001

TIME: 10:45:00

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07242001\I898165.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number